1646

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        RAW SEQUENCE LISTING              DATE: 03/01/2001
        PATENT APPLICATION:  US/09/051,843A     TIME: 12:24:37

        Input Set : A:\sequence.asc
        Output Set: N:\CRF3\03012001\I051843A.raw

  4 <110> APPLICANT: Willson, Tracy
  5        Nicola, Nicos A.
  6        Hilton, Douglas J.
  7        Metcalf, Donald
  8        Zhang, Jian G.
 10 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
 11        ENCODING SAME
 13 <130> FILE REFERENCE: Davies cc
 15 <140> CURRENT APPLICATION NUMBER: 09/051,843A
 16 <141> CURRENT FILING DATE: 1998-06-29
 18 <160> NUMBER OF SEQ ID NOS: 11
 20 <170> SOFTWARE: PatentIn Ver. 2.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1383
 24 <212> TYPE: DNA
 25 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4
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 29 <222> LOCATION: (61)..(1338)
 31 <220> FEATURE:
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71 atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg   108
72 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
73  1              5                  10                  15
75 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca   156
76 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
77              20                  25                  30
79 cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata   204
80 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
81          35                  40                  45
83 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga   252
84 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
85      50                  55                  60
87 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa   300
88 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
89 65                  70                  75                  80
91 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag   348
92 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
93                  85                  90                  95
95 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg   396
96 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
97              100                 105                 110
99 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg   444
100 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
101          115                 120                 125
103 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc   492
104 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
105      130                 135                 140
107 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac   540
108 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
109 145                 150                 155                 160
111 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat   588
112 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
113                 165                 170                 175
115 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa   636
116 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
117              180                 185                 190
119 cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat   684
120 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
121          195                 200                 205
123 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat   732
124 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
125      210                 215                 220
127 gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt   780
128 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
129 225                 230                 235                 240
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Input Set : A:\sequence.asc
Output Set: N:\CRF3\03012001\I051843A.raw

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132 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
133             245             250             255
135 tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat   876
136 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
137             260             265             270
139 att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga   924
140 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
141             275             280             285
143 aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac   972
144 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
145         290             295             300
147 gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt  1020
148 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
149 305             310             315             320
151 gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt  1068
152 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
153             325             330             335
155 aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca  1116
156 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
157             340             345             350
159 gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg  1164
160 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
161         355             360             365
163 ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt  1212
164 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
165     370             375             380
167 aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag  1260
168 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
169 385             390             395             400
171 tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg  1308
172 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
173             405             410             415
175 ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc    1358
176 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
177             420             425
179 tttcttgcct tcaatgtgac cctgt                                      1383
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184 <211> LENGTH: 426
185 <212> TYPE: PRT
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189 <221> NAME/KEY: unsure
190 <222> LOCATION: (21)
191 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
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196 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
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RAW SEQUENCE LISTING   DATE: 03/01/2001
PATENT APPLICATION: US/09/051,843A   TIME: 12:24:37

Input Set : A:\sequence.asc
Output Set: N:\CRF3\03012001\I051843A.raw

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203             20                  25                  30
205 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
206         35                  40                  45
208 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
209     50                  55                  60
211 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
212  65                 70                  75                  80
214 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
215             85                  90                  95
217 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
218             100                 105                 110
220 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
221         115                 120                 125
223 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
224     130                 135                 140
226 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
227 145                 150                 155                 160
229 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
230             165                 170                 175
232 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
233             180                 185                 190
235 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
236         195                 200                 205
238 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
239     210                 215                 220
241 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
242 225                 230                 235                 240
244 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
245             245                 250                 255
247 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
248             260                 265                 270
250 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
251     275                 280                 285
253 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
254     290                 295                 300
256 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
257 305                 310                 315                 320
259 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
260             325                 330                 335
262 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
263             340                 345                 350
265 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
266         355                 360                 365
268 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
269     370                 375                 380
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            RAW SEQUENCE LISTING           DATE: 03/01/2001
            PATENT APPLICATION:  US/09/051,843A     TIME: 12:24:37

            Input Set : A:\sequence.asc
            Output Set: N:\CRF3\03012001\I051843A.raw
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271 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
272 385                 390                 395                 400
274 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
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282 <211> LENGTH: 1383
283 <212> TYPE: DNA
284 <213> ORGANISM: Human IL-13 receptor alpha-chain
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287 <221> NAME/KEY: CDS
288 <222> LOCATION: (61)..(1338)
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294 atg gag tgg ccg gcg cgg ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc  108
295 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
296  1               5               10                  15
298 gcc ggc ggc ggg ggc ggg ggc ggg ggc gcg cct acg gaa act cag cca  156
299 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
300              20                  25                  30
302 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata  204
303 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
304          35                  40                  45
306 tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg  252
307 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
308      50                  55                  60
310 tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa  300
311 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
312  65                  70                  75                  80
314 act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa  348
315 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
316                  85                  90                  95
318 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg  396
319 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
320              100                 105                 110
322 gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg  444
323 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
324          115                 120                 125
326 act gaa ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct  492
327 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
328      130                 135                 140
330 tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac  540
331 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
332 145                 150                 155                 160
334 tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt  588
335 Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
336                 165                 170                 175
338 aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag  636
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PYI

Please Note:
Use of n and/ r Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing t   ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequenc   which presents at least one n or Xaa.

```
           VERIFICATION SUMMARY              DATE: 03/01/2001
           PATENT APPLICATION:  US/09/051,843A     TIME: 12:24:38

           Input Set : A:\sequence.asc
           Output Set: N:\CRF3\03012001\I051843A.raw
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L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:544 M:283 W: Missing Blank Line separator, <220> field identifier
L:544 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:548 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:548 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:560 M:283 W: Missing Blank Line separator, <220> field identifier
L:560 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:568 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:568 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
L:578 M:283 W: Missing Blank Line separator, <220> field identifier
L:578 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:586 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:586 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
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